

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: February 16, 2005, 15:52:54 / Search time 41 Seconds
(without alignment)

1182.762 Million cell updates/sec

Title: US-09-808-124b-6

Sequence: 1 MTINIEDHRLHETSKEPDV.....LPLPEGLQHNCIDNSRLIN 504

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR.79:.*
2: PIR1:.*
3: PIR2:.*
4: PIR3:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2652	98.8	1199	1 GNMVIM	HIV-1 retrovirus
2	2609	97.2	1204	2 S70393	pol polyprotein -
3	2593	96.6	1204	3 S35475	pol polyprotein -
4	2574	95.9	1196	1 GNMVGV	HIV-1 retrovirus
5	2541	94.7	1196	1 GNMVGV	HIV-1 retrovirus
6	2059.5	76.7	1784	2 T10532	gag-pol polyprotein
7	1949.5	72.6	1189	1 GNMVW7	HIV-1 retrovirus
8	1893	70.5	1165	1 GNMVGL	HIV-1 retrovirus
9	1888.5	70.4	1046	1 GNMVCE	pol polyprotein -
10	1372	51.1	843	1 GNMVCE	pol polyprotein -
11	1130	42.1	559	2 A46311	gag-pol polyprotein
12	778.5	29.0	1751	2 T09394	pol polyprotein
13	669	24.9	476	2 S04842	probable pol prote
14	433	16.1	122	4 T01781	pol polyprotein
15	431.5	16.1	1157	1 GNMVJL	pol polyprotein -
16	430.5	16.0	958	2 S18738	pol protein - siml
17	428.5	16.0	958	2 S15566	hypothetical prote
18	416	15.5	1236	2 B35329	retrovirus-related
19	412	15.4	1059	2 B24872	probable retrovira
20	403	15.0	1611	2 G84493	probable retrovira
21	399	14.9	949	2 D84487	pro-pol-dutpase po
22	397	14.8	1182	2 T29097	pol polyprotein -
23	381.5	14.2	886	1 T07863	probable polyprote
24	377.5	14.1	871	2 T07863	blatopia polyprot
25	375	14.0	1333	2 S38635	retrovirus-related
26	374.5	14.0	1058	1 GNFPI7	pol protein - frul
27	373	13.9	1040	1 S34639	gag, pol and env p
28	370.5	13.8	2272	2 T18572	pol polyprotein ho
29	365	13.6	1045	2 S23570	

30	364.5	13.6	1060	2 T43046	retrovirus-related
31	357	13.3	1745	2 S44816	P4482.1 protein -
32	351	13.1	1313	2 T29193	hypothetical prote
33	348.5	13.0	1398	2 T18350	probable pol poly
34	343.5	12.8	1542	2 T17459	pol polyprotein -
35	340	12.7	1009	2 S64734	retrovirus-related
36	337	12.6	1295	2 S60179	pol polyprotein ho
37	335	12.5	895	2 S35429	pol polyprotein -
38	335	12.5	982	1 GNLJH2	pol polyprotein -
39	335	12.5	1217	2 T13996	pol protein - frul
40	335	12.5	1240	2 T04193	hypothetical prote
41	334.5	12.5	895	2 GNFVIR	pol polyprotein -
42	333	12.4	896	2 S48613	pol polyprotein -
43	332.5	12.4	1603	2 A48613	gag/pol polyprotei
44	332	12.4	896	2 S48613	pol polyprotein -
45	330.5	12.3	399	4 A45689	retrovirus-related

ALIGNMENTS

RESULT 1

GNMVIM HIV-1 retrovirus (EC 3.4.23.16) - Moloney murine leukemia virus

N/Contains: nuclease (EC 3.1.-.-); retrovirus (EC 3.4.23.16); RNA-directed DNA polymer

C/Species: Moloney murine leukemia virus

A/Note: host Mus spp. (mouse)

C/date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 03-Jun-2002

C/accession: A03956

R/Shimick, T.M.; Lerner, R.A.; Sutcliffe, J.G.

Nature 293, 545-548, 1981

A/Title: Nucleotide sequence of Moloney murine leukemia virus.

A/Reference number: A93265; MUID:82035843; PMID:6169994

A/Accession: A03956

A/Molecule type: genomic RNA

A/Residues: 1-1199 (SHI)

A/Experimental source: clone pMLV-1

A/Note: the pol polyprotein contains reverse transcriptase (about 80,000 daltons) and i

t yet been defined

C/Comment: This protein is synthesized as a gag-pol polyprotein.

C/Genetics:

A/Gene: pol

C/Superfamily: pol polyprotein

C/Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase; polyprotein; revers

F.3-102/Product: retrovirus #status predicted <RTP>

F.27/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 98.8%; Score 2652; DB 1; Length 1199;

Best Local Similarity 99.8%; Pred. No. 6.7e-187;

Matches 497; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTINIEDHRLHETSKEPDVSLGTSWLSDFPQAMETGGMGLAVQAAPLIPLKATSTPV	60
DB	120	LTINIEDHRLHETSKEPDVSLGTSWLSDFPQAMETGGMGLAVQAAPLIPLKATSTPV	179
QY	61	SIKQYPMQEARLGIKPIQRLDQGLVPCSPMNTPLPVKKGTNDYRPVQDLREVN	120
DB	180	SIKQYPMQEARLGIKPIQRLDQGLVPCSPMNTPLPVKKGTNDYRPVQDLREVN	239
QY	121	KRVEDIHTVPNPVNLGLPPSHQWTVLIDKAFCLRLHPTSPQPLFAEWRDPEMGI	180
DB	240	KRVEDIHTVPNPVNLGLPPSHQWTVLIDKAFCLRLHPTSPQPLFAEWRDPEMGI	299
QY	131	SGQLTWTLPGGFKNSPLFPBALHRLADRIQHPDILLYOVYDILLAAITSELDCCOG	240
DB	300	SGQLTWTLPGGFKNSPLFPBALHRLADRIQHPDILLYOVYDILLAAITSELDCCOG	359
QY	241	TRALLQITGNIGYRSASAKAIOICQKQVYLGILLKEGQWLTFAKRTVMGPTPTKTRQ	300
DB	360	TRALLQITGNIGYRSASAKAIOICQKQVYLGILLKEGQWLTFAKRTVMGPTPTKTRQ	419
QY	301	LREFTGAGFCRLWITGFAEWAAPLYLTKGTTLFNMGPDOCKAYOEIKOALLTPALCL	360

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OM protein - protein search, using sw model

Run on: February 16, 2005, 15:52:54 ; Search time 181 Seconds

(without alignments)
1425.900 Million cell updates/sec

Title: US-09-808-124B-6

Perfect score: 2684
Sequence: 1 MTLNIEDERHRLHETSKEDPV.....LPLEBGLQHNCIDNSRLIN 504

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_prot:*
2: uniprot_crembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2652	98.8	1199	1 POL_MLVMO	P03355 moloney mur
2	2652	98.8	1737	2 O92808	O92808 moloney mur
3	2636	98.2	1738	3 O8UN00	O8UN00 moloney mur
4	2614	97.4	1204	2 O41250	O41250 rauscher mu
5	2612	97.3	1736	2 O72076	O72076 amphotropic
6	2609	97.2	1204	1 POL_MLVFF	P26809 friend muri
7	2605	97.1	1204	2 O9YK99	O9YK99 murine leuk
8	2593	96.6	1204	1 POL_MLVFP	P26808 friend muri
9	2587	96.4	1738	2 O39735	O39735 friend muri
10	2583	96.2	1204	1 POL_MLVFS	P26810 friend muri
11	2579	96.1	1733	2 O9E7M1	O9E7M1 dg-75 murin
12	2576	96.0	1734	2 O9E7M7	O9E7M7 murine leuk
13	2571	95.8	1734	2 O948E2	O948E2 murine leuk
14	2568	95.7	1196	1 POL_MLVAV	P03356 akv murine
15	2567.5	95.7	1736	2 O83362	O83362 murine leuk
16	2567	95.6	1734	2 P70355	P70355 mus musculu
17	2552	95.1	1196	2 O90RL4	O90RL4 murine leuk
18	2541	94.7	1196	1 POL_MLVVD	P11227 radiation m
19	2504	93.3	1180	2 O9WHV7	O9WHV7 murine leuk
20	2295	89.2	1038	2 O83398	O83398 murine leuk
21	2198.5	81.9	626	2 O72L06	O72L06 recombinant
22	2191.5	81.7	626	2 O72L04	O72L04 recombinant
23	2181.5	81.3	1204	2 O72K27	O72K27 recombinant
24	2127.5	79.3	1204	2 O72K29	O72K29 recombinant
25	2125.5	79.2	1204	2 O72K25	O72K25 recombinant
26	2075.5	77.4	1786	2 O88811	O88811 murine leuk
27	2058.5	76.7	1784	2 O88521	O88521 murine leuk
28	1945.5	72.6	1189	1 POL_BAEVM	P10722 baboon endo
29	1945.5	72.5	868	2 O73505	O73505 porcine endo
30	1945.5	72.5	2376	2 O901X5	O901X5 porcine endo
31	1944.5	72.4	1146	2 O8UM96	O8UM96 porcine endo

RESULT 1	ID	POL_MLVMO	STANDARD	PRT	1199 AA.	ALIGNMENTS
AC	P03355					O8J4V8 porcine end
DT	21-JUL-1986	(Rel. 01, Created)				O8J4V6 porcine end
DT	01-FEB-1996	(Rel. 33, Last sequence update)				O90RL6 porcine end
DT	25-OCT-2004	(Rel. 45, Last annotation update)				O901X4 porcine end
DE	Pol polyprotein [Contains: Protease (EC 3.4.23.-); Reverse transcriptase/RNase H (EC 2.7.7.49) (EC 3.1.26.4) (RT); Integrase (IN)].					O901X3 porcine end
GN	Name=POL;					O9XSN8 porcine end
OC	Moloney murine leukemia virus.					O9XSN8 sus scrofa
OS	Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.					O8UM99 porcine end
OX	NCBI_Taxid=11801;					O90RL9 porcine end
RN	[1]					O8UM95 porcine end
RP	SEQUENCE FROM N.A. (CLONE PMLV-1).					O901X1 porcine end
RX	MEDLINE=82035843; PubMed=6169994;					O901X1 porcine end
RA	Shimnick R.M., Lerner R.A., Sutcliffe J.G.;					O901X1 porcine end
RT	"Nucleotide sequence of Moloney murine leukemia virus."					O901X1 porcine end
RL	Nature 293:543-548 (1981).					O901X1 porcine end
RN	[2]					O901X1 porcine end
RX	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 130-394.					O901X1 porcine end
RA	MEDLINE=96097395; PubMed=8535782; DOI=10.1016/S0969-2126(01)00223-4;					O901X1 porcine end
RT	Georgiadis M.M., Jessen S.M., Ogata C.M., Telenitsky A., Goff S.P.,					O901X1 porcine end
RL	Hendrickson W.A.;					O901X1 porcine end
CC	"Mechanistic implications from the structure of a catalytic fragment of Moloney murine leukemia virus reverse transcriptase."					O901X1 porcine end
CC	Structure 3:879-892 (1995).					O901X1 porcine end
CC	- FUNCTION: During replicative cycle of retroviruses, the reverse-					O901X1 porcine end
CC	the viral integrase enzyme. RNase H activity is associated with					O901X1 porcine end
CC	the reverse transcriptase.					O901X1 porcine end
CC	- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-					O901X1 porcine end
CC	phosphomonoester.					O901X1 porcine end
CC	- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate					O901X1 porcine end
CC	+ (dNp) (N).					O901X1 porcine end
CC	- PTM: Specific enzymatic cleavages in vivo yield mature proteins.					O901X1 porcine end
CC	- MISCELLANEOUS: This protein is synthesized as a Gag-Pol					O901X1 porcine end
CC	polyprotein.					O901X1 porcine end
CC	- SIMILARITY: Belongs to the retroviruses Pol polypeptide family.					O901X1 porcine end
CC	- SIMILARITY: Contains 1 peptidase A2 domain.					O901X1 porcine end
CC	- SIMILARITY: Contains 1 reverse transcriptase domain.					O901X1 porcine end
CC	- SIMILARITY: Contains 1 RNase H domain.					O901X1 porcine end
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration					O901X1 porcine end
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -					O901X1 porcine end
CC	the European Bioinformatics Institute. There are no restrictions on its					O901X1 porcine end
CC	use by non-profit institutions as long as its content is in no way					O901X1 porcine end
CC	modified and this statement is not removed. Usage by and for commercial					O901X1 porcine end
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/					O901X1 porcine end
CC	or send an email to license@isb-sib.ch).					O901X1 porcine end
DR	EMBL, J02255; -; NOT ANNOTATED_CDS.					O901X1 porcine end
DR	PDB, 1D1U; X-ray; A-I44-398.					O901X1 porcine end

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OM protein - protein search, using sw model

Run on: February 16, 2005, 15:53:10 ; Search time 43 Seconds

(without alignments)
874,956 Million cell updates/sec

Title: US-09-808-124B-6

Perfect score: 2684
Sequence: 1 MTLNIEDHRLHETSKPEPVY.....LPPEBGLQHNCLDNLRLIN 504

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/SA_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/SB_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/SA_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/SB_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/PCUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2652	98.8	1737	4	US-09-309-572-13 Sequence 13, Appl
2	2652	98.8	1737	4	US-09-718-096-13 Sequence 13, Appl
3	2650	98.7	1079	2	US-08-929-967-8 Sequence 8, Appl
4	2611	97.3	665	2	US-08-929-967-7 Sequence 7, Appl
5	2027	75.5	379	3	US-09-603-185-6 Sequence 6, Appl
6	1944.5	72.4	1194	4	US-09-171-553B-5 Sequence 5, Appl
7	1903	70.9	1203	3	US-09-075-272-4 Sequence 4, Appl
8	985.5	36.7	654	4	US-08-979-847B-91 Sequence 91, Appl
9	985.5	36.7	768	4	US-08-979-847B-89 Sequence 89, Appl
10	978.5	36.5	683	4	US-08-979-847B-198 Sequence 198, App
11	978.5	36.5	683	4	US-08-979-847B-200 Sequence 200, App
12	975.5	36.3	683	4	US-08-979-847B-208 Sequence 208, App
13	975.5	36.3	683	4	US-08-979-847B-210 Sequence 210, App
14	915.5	34.1	768	3	US-09-120-653D-5 Sequence 5, Appl
15	345	12.9	995	5	PCT-US95-04910-14 Sequence 14, Appl
16	337	12.6	65	6	5320958-16 Patent No. 5320958
17	337	12.6	65	6	5320958-16 Patent No. 5320958
18	336.5	12.5	917	4	US-08-259-451-11 Sequence 11, Appl
19	319.5	11.9	146	4	US-08-979-847B-209 Sequence 209, App
20	318.5	11.9	146	4	US-08-979-847B-133 Sequence 133, App
21	317.5	11.8	146	4	US-08-979-847B-132 Sequence 132, App
22	317.5	11.8	146	4	US-08-979-847B-202 Sequence 202, App
23	316	11.8	1122	4	US-09-248-796A-16374 Sequence 16374, A
24	309.5	11.5	146	4	US-08-979-847B-134 Sequence 134, App
25	288.5	10.7	1055	2	US-08-659-251-5 Sequence 5, Appl
26	288.5	10.7	1055	2	US-09-256-490-5 Sequence 5, Appl
27	288.5	10.7	1055	5	PCT-US96-11445-5 Sequence 5, Appl

28	282	10.5	143	4	US-08-979-847B-199	Sequence 199, App
29	282	10.5	143	4	US-08-979-847B-203	Sequence 203, App
30	281.5	10.5	1150	3	US-09-238-303-9	Sequence 9, Appl
31	281.5	10.5	1150	4	US-09-946-239-9	Sequence 9, Appl
32	281	10.5	1802	3	US-09-322-478-18	Sequence 18, Appl
33	281	10.5	1802	4	US-09-586-106D-18	Sequence 18, Appl
34	280.5	10.5	260	6	5320958-4	Patent No. 5320958
35	280.5	10.5	260	6	5320958-4	Patent No. 5320958
36	277	10.3	143	4	US-08-979-847B-141	Sequence 141, App
37	275	10.2	143	4	US-08-979-847B-139	Sequence 139, App
38	274	10.2	143	4	US-08-979-847B-140	Sequence 140, App
39	273	10.2	3080	6	5223423-4	Patent No. 5223423
40	273	10.2	3080	6	5223423-4	Patent No. 5223423
41	261.5	9.7	1031	3	US-08-811-682-15	Sequence 15, Appl
42	258.5	9.6	146	4	US-08-979-847B-204	Sequence 204, App
43	249	9.3	1018	4	US-09-206-551-46	Sequence 46, App
44	244.5	9.1	560	4	US-10-205-641-1	Sequence 1, Appl
45	244.5	9.1	850	4	US-09-952-060-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1									
US-09-309-572-13									
Sequence 13, Application US/09309572									
Patent No. 6440730									
GENERAL INFORMATION:									
APPLICANT: Heinrich-Pette-Institut									
TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV									
FILE REFERENCE: P50489									
CURRENT APPLICATION NUMBER: US/09/309,572									
CURRENT FILING DATE: 1999-05-11									
EARLIER APPLICATION NUMBER: DE 198 56 463									
EARLIER FILING DATE: 1998-11-26									
NUMBER OF SEQ ID NOS: 24									
SOFTWARE: Patentin Ver. 2.0									
SEQ ID NO 13									
LENGTH: 1737									
TYPE: PRT									
ORGANISM: Moloney murine leukemia virus									
FEATURE:									
OTHER INFORMATION: gag-pol protein									
US-09-309-572-13									
Query Match									
Best Local Similarity 98.8%; Score 2652; DB 4; Length 1737;									
Matches 497; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MTLNIEDHRLHETSKPEPVYLSGSTWLSDFQANAETGGMGLANVQAPLIITLKATSTPV	60						
DB	658	LTNIEDHRLHETSKPEPVLSGSTWLSDFQANAETGGMGLANVQAPLIITLKATSTPV	717						
QY	61	SIKQYPMQSEARLGIKPHIQRLDQGIIVPCQSPWNTPLPVYKKGTDYRPVQDLREVN	120						
DB	718	SIKQYPMQSEARLGIKPHIQRLDQGIIVPCQSPWNTPLPVYKKGTDYRPVQDLREVN	777						
QY	121	KRVEDIHPTVNPVNLISGLPPSHQWTVLDKQAFCLRLHPTSPQLFAFEMRDPENGI	180						
DB	778	KRVEDIHPTVNPVNLISGLPPSHQWTVLDKQAFCLRLHPTSPQLFAFEMRDPENGI	837						
QY	181	SGQLTWLTPGQFNKSPFLFDEALHRLDADRIQHPDILILQYVDDLLAATSELDCCQG	240						
DB	838	SGQLTWLTPGQFNKSPFLFDEALHRLDADRIQHPDILILQYVDDLLAATSELDCCQG	897						
QY	241	TRALLQTLGNIGYASAKKQICQKQVYLYLKEGQWLTARKEVTPMGQPTPKTPRQ	300						
DB	898	TRALLQTLGNIGYASAKKQICQKQVYLYLKEGQWLTARKEVTPMGQPTPKTPRQ	957						
QY	301	LREELGTAGPRLMIIPGABMAAPLYLTKTGTLFPMNGPDQKAYOETIKQALLTPALGL	360						
DB	958	LREELGTAGPRLMIIPGABMAAPLYLTKTGTLFPMNGPDQKAYOETIKQALLTPALGL	1017						